

# ALIGNMENT

LOCUS AX076272 6995 bp DNA linear PAT 06-FEB-2001  
 DEFINITION Sequence 1 from Patent WO0104325.  
 ACCESSION AX076272  
 VERSION AX076272.1 GI:12710897  
 KEYWORDS .  
 SOURCE Corynebacterium glutamicum.  
 ORGANISM Corynebacterium glutamicum  
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 Actinomycetales; Corynebacterineae; Corynebacteriaceae;  
 Corynebacterium.  
 REFERENCE 1 (bases 1 to 6995)  
 AUTHORS Dunican,L.K., Stapelton,C., Burke,K. and Moeckel,B.  
 TITLE Nucleotide sequences for the tal gene  
 JOURNAL Patent: WO 0104325-A 1 18-JAN-2001;  
 Degussa-Huels Aktiengesellschaft (DE) ; National University of  
 Ireland (IE)

Query Match 100.0%; Score 828; DB 6; Length 6995;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-196;  
 Matches 828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAGGAGCTTCGCCACATGGATCCAGATTTGGGCTACCAGCACGCACTATCCGGCTTGTC 60
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Db    6093 GAGGAGCTTCGCCACATGGATCCAGATTTGGGCTACCAGCACGCACTATCCGGCTTGTC 6152

Qy     61 AGCGTCAAGCTGGAAACCGTCTAAGGAGAAATACAACACTATGGTTGATGTAGTACGCGC 120
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Db    6153 AGCGTCAAGCTGGAAACCGTCTAAGGAGAAATACAACACTATGGTTGATGTAGTACGCGC 6212

Qy    121 ACGCGATACTGAAGATTGTTGTCACAGGCTGCCTCCAAATTCATTGAGGTTGTTGAAGC 180
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Db    6213 ACGCGATACTGAAGATTGTTGTCACAGGCTGCCTCCAAATTCATTGAGGTTGTTGAAGC 6272

Qy    181 AGCAACTGCCAATAATGGCACCGCACAGGTAGTGCTCACCAGGTGGTGGCGCCGGCATCAA 240
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Db    6273 AGCAACTGCCAATAATGGCACCGCACAGGTAGTGCTCACCAGGTGGTGGCGCCGGCATCAA 6332

Qy    241 GTTGCTGGAAAAGCTCAGCGTTGATGCGGCTGACCTTGCCTGGGATCGCATTTCATGTGTT 300
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Db    6333 GTTGCTGGAAAAGCTCAGCGTTGATGCGGCTGACCTTGCCTGGGATCGCATTTCATGTGTT 6392

Qy    301 CTTGCGCGATGAGCGCAATGTCCCTGTCAGTGATTCTGAGTCCAATGAGGGCCAGGCTCG 360
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Db    6393 CTTGCGCGATGAGCGCAATGTCCCTGTCAGTGATTCTGAGTCCAATGAGGGCCAGGCTCG 6452

Qy    361 TGAGGCACTGTTGTCCAAGGTTTCTATCCCTGAAGCCAACATTCACGGATATGGTCTCGG 420
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Db    6453 TGAGGCACTGTTGTCCAAGGTTTCTATCCCTGAAGCCAACATTCACGGATATGGTCTCGG 6512

Qy    421 CGACGTAGATCTTGCAGAGGCAGCCCGCGCTTACGAAGCTGTGTTGGATGAATTCGCACC 480
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Db    6513 CGACGTAGATCTTGCAGAGGCAGCCCGCGCTTACGAAGCTGTGTTGGATGAATTCGCACC 6572

Qy    481 AAACGGCTTTGATCTTCACCTGCTCGGCATGGGTGGCGAAGGCCATATCAACTCCCTGTT 540
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Db    6573 AAACGGCTTTGATCTTCACCTGCTCGGCATGGGTGGCGAAGGCCATATCAACTCCCTGTT 6632
  
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Qy	541	CCCTCACACCGATGCAGTCAAGGAATCCTCCGCAAAGGTCATCGCGGTGTTTGATTCCCC	600
Db	6633	CCCTCACACCGATGCAGTCAAGGAATCCTCCGCAAAGGTCATCGCGGTGTTTGATTCCCC	6692
Qy	601	TAAGCCTCCTTCAGAGCGTGCAACTCTAACCCTTCTGCGGTTCACTCCGCAAAGCGCGT	660
Db	6693	TAAGCCTCCTTCAGAGCGTGCAACTCTAACCCTTCTGCGGTTCACTCCGCAAAGCGCGT	6752
Qy	661	GTGGTTGCTGGTTTCTGGTGCGGAGAAGGCTGAGGCAGCTGCGGCGATCGTCAACGGTGA	720
Db	6753	GTGGTTGCTGGTTTCTGGTGCGGAGAAGGCTGAGGCAGCTGCGGCGATCGTCAACGGTGA	6812
Qy	721	GCCTGCTGTTGAGTGGCCTGCTGCTGGAGCTACCGGATCTGAGGAAACGGTATTGTTCTT	780
Db	6813	GCCTGCTGTTGAGTGGCCTGCTGCTGGAGCTACCGGATCTGAGGAAACGGTATTGTTCTT	6872
Qy	781	GGCTGATGATGCTGCAGGAAATCTCTAAGCAGCGCCAGCTCTAACAAG	828
Db	6873	GGCTGATGATGCTGCAGGAAATCTCTAAGCAGCGCCAGCTCTAACAAG	6920